

RAW SEQUENCE LISTING

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Application Serial Number: 10/563,166

Source: IFWP

Date Processed by STIC: 1/13/06

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IFWP

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/563,166

TIME: 10:52:05

Input Set : E:\11711-001-999 (Sequence).txt

Output Set: N:\CRF4\01132006\J563166.raw

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5 <110> APPLICANT: Hidai, Chiaki
7 <120> TITLE OF INVENTION: Protein Capable of Deposition onto Extracellular Matrix
9 <130> FILE REFERENCE: 11711-001-999(P03-0057PCT)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/563,166
C--> 12 <141> CURRENT FILING DATE: 2005-12-29
14 <150> PRIOR APPLICATION NUMBER: JP2003-188598
15 <151> PRIOR FILING DATE: 2003-06-30
17 <160> NUMBER OF SEQ ID NOS: 26
19 <170> SOFTWARE: PatentIn version 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2303
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (619)..(2061)
31 <400> SEQUENCE: 1
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34 ttcccagtggt ccttgatatt taaactgatt cctgccacca ggtccttggg ccaccctgtc      120
36 cctgcgtctc atatttctgc atgctgcttt gtttgatat agtgcgctcc tggcctcagg      180
38 ctgcgtcccc tccagctctc gcttcattgt tctccaagtc agaagcccc gcacccgccc      240
40 cgcagcagcg tgagccgtag tctactgctg cgccttcgcc tgcgtgcgcg cacggaatc      300
42 ggggagccag gaacccaagg agccgccgtc cgccctcgct gcctctgcta gaccactcgc      360
44 agccccagcc tctctcaagc gcaccaccc cgcgcaccc cagctcaggc gaagctggag      420
46 tgagggtgaa tcaccctttc tctagggcca ccactctttt atcgcccttc ccaagatttg      480
48 agaagcgctg cgggaggaaa gacgtcctct tgatctctga cagggcgggg tttactgctg      540
50 tcctgcaggc gcgcctcgcc tactgtgccc tccgctacga ccccggaacca gcccagggtca      600
52 cgtccgtgag aagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt      651
53                               Met Lys His Leu Val Ala Ala Trp Leu Leu Val
54                               1           5           10
56 gga ctc agc ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac      699
57 Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
58                               15           20           25
60 ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat      747
61 Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
62                               30           35           40
64 gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc      795
65 Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
66                               45           50           55
68 tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca      843
69 Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
70 60                               65           70           75
72 ggt ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata      891

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73 Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile
74          80          85          90
76 agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt      939
77 Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
78          95          100          105
80 cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt      987
81 Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
82          110          115          120
84 gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct      1035
85 Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala
86          125          130          135
88 aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa      1083
89 Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln
90 140          145          150          155
92 tat aaa tgc tct ggg cca ttg gga atc gaa ggt ggg atc ata tct aat      1131
93 Tyr Lys Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn
94          160          165          170
96 cag caa atc aca gct tca tct act cac cga gct ctt ttt gga ctc cgg      1179
97 Gln Gln Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Arg
98          175          180          185
100 aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat      1227
101 Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn
102          190          195          200
104 gcc tgg aca gct gct gaa aat gac aga tgg cca tgg att cag ata aat      1275
105 Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn
106          205          210          215
108 ttg caa aga aaa atg aga gtc act ggt gtt att acc caa gga gca aaa      1323
109 Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
110 220          225          230          235
112 agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc tac agc      1371
113 Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser
114          240          245          250
116 aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc aat gaa      1419
117 Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
118          255          260          265
120 gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat gct aat      1467
121 Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn
122          270          275          280
124 tct ttc aca ccc cca atc aaa gct cag tat gta aga ctc tac ccc caa      1515
125 Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
126          285          290          295
128 att tgt cga agg cat tgt act tta aga atg gaa ctt ctt ggc tgt gag      1563
129 Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
130 300          305          310          315
132 ctc tca ggc tgt tca gaa cct ttg ggg atg aaa tca ggg cat ata caa      1611
133 Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
134          320          325          330
136 gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac atg gac      1659
137 Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp

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138          335          340          345
140 atg ttt act tgg gaa cca agg aaa gcc agg ctg gac aag caa ggc aaa      1707
141 Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
142          350          355          360
144 gta aat gcc tgg act tcc ggc cat aac gac cag tca caa tgg tta cag      1755
145 Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
146          365          370          375
148 gtt gat ctt ctt gtc cct act aag gtg aca ggc atc att aca caa gga      1803
149 Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
150 380          385          390          395
152 gct aaa gat ttt ggt cac gtg cag ttt gtt ggg tca tac aaa cta gct      1851
153 Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
154          400          405          410
156 tac agc aat gat gga gaa cac tgg atg gtg cac cag gat gaa aaa cag      1899
157 Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
158          415          420          425
160 agg aaa gac aag gtt ttt caa ggc aat ttt gac aat gac act cac agg      1947
161 Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
162          430          435          440
164 aaa aat gtc atc gac cct ccc atc tat gca cga ttc ata aga atc ctt      1995
165 Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
166          445          450          455
168 cct tgg tcc tgg tat gga agg atc act ctg cgg tca gag ctg ctg ggc      2043
169 Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly
170 460          465          470          475
172 tgc gca gag gag gaa tga agtgcggggc cgcacatccc acaatgcttt      2091
173 Cys Ala Glu Glu
174          480
176 tctttattttt cctataagta tctccacgaa atgaactgtg tgaagctgat ggaaactgca      2151
178 tttgtttttt tcaaagtgtt caaattatgg taggctactg actgtctttt taggagttct      2211
180 aagcttgccct ttttaataat ttaatttggg ttcccttgct caactctctt atgtaatatc      2271
182 acactgtctg tgagttactc ttcttggtct ct      2303
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 480
187 <212> TYPE: PRT
188 <213> ORGANISM: Mus musculus
190 <400> SEQUENCE: 2
192 Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
193 1          5          10          15
196 Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
197          20          25          30
200 Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
201          35          40          45
204 Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
205          50          55          60
208 Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
209 65          70          75          80
212 Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
213          85          90          95

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216 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
217      100      105      110
220 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
221      115      120      125
224 Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
225      130      135      140
228 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
229 145      150      155      160
232 Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
233      165      170      175
236 Ser Ser Thr His Arg Ala Leu Phe Gly Leu Arg Lys Trp Tyr Pro Tyr
237      180      185      190
240 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
241      195      200      205
244 Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
245      210      215      220
248 Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
249 225      230      235      240
252 Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
253      245      250      255
256 Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
257      260      265      270
260 Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
261      275      280      285
264 Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
265      290      295      300
268 Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
269 305      310      315      320
272 Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
273      325      330      335
276 Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
277      340      345      350
280 Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
281      355      360      365
284 Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
285      370      375      380
288 Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
289 385      390      395      400
292 His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
293      405      410      415
296 Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
297      420      425      430
300 Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
301      435      440      445
304 Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
305      450      455      460
308 Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
309 465      470      475      480
312 <210> SEQ ID NO: 3

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Input Set : E:\11711-001-999 (Sequence).txt

Output Set: N:\CRF4\01132006\J563166.raw

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313 <211> LENGTH: 393
314 <212> TYPE: DNA
315 <213> ORGANISM: Mus musculus
318 <220> FEATURE:
319 <221> NAME/KEY: CDS
320 <222> LOCATION: (1)..(393)
322 <400> SEQUENCE: 3
323 ata aat ttg caa aga aaa atg aga gtc act ggt gtt att acc caa gga      48
324 Ile Asn Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly
325 1      5      10      15
327 gca aaa agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc      96
328 Ala Lys Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala
329      20      25      30
331 tac agc aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc      144
332 Tyr Ser Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr
333      35      40      45
335 aat gaa gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat      192
336 Asn Glu Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr
337      50      55      60
339 gct aat tct ttc aca ccc cca atc aaa gct cag tat gta aga ctc tac      240
340 Ala Asn Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr
341 65      70      75      80
343 ccc caa att tgt cga agg cat tgt act tta aga atg gaa ctt ctt ggc      288
344 Pro Gln Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly
345      85      90      95
347 tgt gag ctc tca ggc tgt tca gaa cct ttg ggg atg aaa tca ggg cat      336
348 Cys Glu Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His
349      100      105      110
351 ata caa gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac      384
352 Ile Gln Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn
353      115      120      125
355 atg gac atg      393
356 Met Asp Met
357      130
360 <210> SEQ ID NO: 4
361 <211> LENGTH: 131
362 <212> TYPE: PRT
363 <213> ORGANISM: Mus musculus
365 <400> SEQUENCE: 4
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368 1      5      10      15
371 Ala Lys Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala
372      20      25      30
375 Tyr Ser Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr
376      35      40      45
379 Asn Glu Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr
380      50      55      60
383 Ala Asn Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr
384 65      70      75      80

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VERIFICATION SUMMARY

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Input Set : E:\11711-001-999 (Sequence).txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date